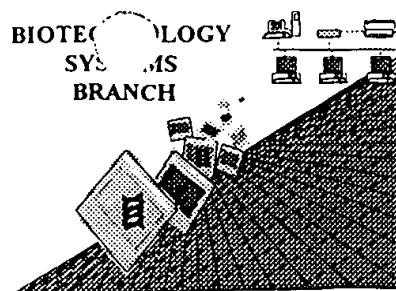


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/807,949
Source: PCT 09
Date Processed by STIC: 5-7-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/807,949

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 ✓ _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 _____ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,949

DATE: 05/07/2001

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

3 <110> APPLICANT: Zavada, Jan
 4 Pastorekova, Silvia
 5 Pastorek, Jaromir
 7 <120> TITLE OF INVENTION: MN Gene and Protein
 9 <130> FILE REFERENCE: D-0021.5 PCT
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/807,949
 C--> 12 <141> CURRENT FILING DATE: 2001-04-19
 14 <150> PRIOR APPLICATION NUMBER: 09/177,776
 15 <151> PRIOR FILING DATE: 1998-10-23
 17 <150> PRIOR APPLICATION NUMBER: 09/178,115
 18 <151> PRIOR FILING DATE: 1998-10-23
 20 <160> NUMBER OF SEQ ID NOS: 143
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1522
 26 <212> TYPE: DNA
 27 <213> ORGANISM: HUMAN
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (13)..(1389)
 33 <220> FEATURE:
 34 <221> NAME/KEY: mat_peptide
 35 <222> LOCATION: (124)..(1389)
 37 <400> SEQUENCE: 1
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 39 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu
 40 -35 -30 -25
 42 atc ccg gcc cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg 99
 43 Ile Pro Ala Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu
 44 -20 -15 -10
 46 ctg ctt ctg atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag 147
 47 Leu Leu Leu Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu
 48 -5 -1 1 5
 50 gat tcc ccc ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc 195
 51 Asp Ser Pro Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly
 52 10 15 20
 54 gag gag gat ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca 243
 55 Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro
 56 25 30 35 40
 58 ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag 291
 59 Pro Gly Glu Glu Asp Leu Pro Gly Glu Asp Leu Pro Gly Glu Glu
 60 45 50 55
 62 gat cta cct gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag 339
 63 Asp Leu Pro Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys
 64 60 65 70
 66 tta gag gat cta cct act gtt gag gct cct gga gat cct caa gaa ccc 387
 67 Leu Glu Asp Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro

Does Not Comply
 Corrected Diskette Needed

pp. 4-5

RAW SEQUENCE LISTING

DATE: 05/07/2001

PATENT APPLICATION: US/09/807,949

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

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70	cag aat aat gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg	435		
71	Gln Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp			
72	90 95 100			
74	cgc tat gga ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg	483		
75	Arg Tyr Gly Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala			
76	105 110 115 120			
78	ggc cgc ttc cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc	531		
79	Gly Arg Phe Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe			
80	125 130 135			
82	tgc ccg gcc ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg	579		
83	Cys Pro Ala Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro			
84	140 145 150			
86	ctc cca gaa ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc	627		
87	Leu Pro Glu Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr			
88	155 160 165			
90	ctg cct cct ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg	675		
91	Leu Pro Pro Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg			
92	170 175 180			
94	gct ctg cag ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tgc	723		
95	Ala Leu Gln Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser			
96	185 190 195 200			
98	gag cac act gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt	771		
99	Glu His Thr Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val			
100	205 210 215			
102	cac ctc agc acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg	819		
103	His Leu Ser Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro			
104	220 225 230			
106	gga ggc ctg gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa	867		
107	Gly Gly Leu Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu			
108	235 240 245			
110	aac agt gcc tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag	915		
111	Asn Ser Ala Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu			
112	250 255 260			
114	gaa ggc tca gag act cag gtc cca gga ctg gac ata tct gca ctc ctg	963		
115	Glu Gly Ser Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu			
116	265 270 275 280			
118	ccc tct gac ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca	1011		
119	Pro Ser Asp Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr			
120	285 290 295			
122	ccg ccc tgt gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg	1059		
123	Pro Pro Cys Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val			
124	300 305 310			
126	atg ctg agt gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga	1107		
127	Met Leu Ser Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly			
128	315 320 325			
130	cct ggt gac tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg	1155		
131	Pro Gly Asp Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu			
132	330 335 340			

RAW SEQUENCE LISTING

DATE: 05/07/2001

PATENT APPLICATION: US/09/807,949

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

```

134 aat ggg cga gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt 1203
135 Asn Gly Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser
136 345 350 355 360
138 cct cgg gct gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt 1251
139 Pro Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly
140 365 370 375
142 gac atc cta gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc 1299
143 Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val
144 380 385 390
146 gcg ttc ctt gtg cag atg aga agg cag cac aga agg gga acc aaa ggg 1347
147 Ala Phe Leu Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly
148 395 400 405
150 ggt gtg agc tac cgc cca gca gag gta gcc gag act gga gcc 1389
151 Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
152 410 415 420
154 tagaggctgg atcttgagaga atgtgagaag ccagccagag gcattctgagg gggagccggt 1449
156 aactgtcctg tctgtctcat tatgccactt ccttttaact gccagaagaat tttttaaaat 1509
158 aaatatattat aat 1522
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 459
163 <212> TYPE: PRT
164 <213> ORGANISM: HUMAN
166 <400> SEQUENCE: 2
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168 -35 -30 -25
170 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
171 -20 -15 -10
173 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
174 -5 -1 1 5 10
176 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
177 15 20 25
179 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
180 30 35 40
182 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
183 45 50 55
185 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
186 60 65 70 75
188 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
189 80 85 90
191 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
192 95 100 105
194 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
195 110 115 120
197 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
198 125 130 135
200 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
201 140 145 150 155
203 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
204 160 165 170

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,949

DATE: 05/07/2001

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

```

206 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
207          175          180          185
209 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
210          190          195          200
212 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
213          205          210          215
215 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
216 220          225          230          235
218 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
219          240          245          250
221 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
222          255          260          265
224 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
225          270          275          280
227 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
228          285          290          295
230 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
231 300          305          310          315
233 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
234          320          325          330
236 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
237          335          340          345
239 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
240          350          355          360
242 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
243          365          370          375
245 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
246 380          385          390          395
248 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
249          400          405          410
251 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
252          415          420

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256 <210> SEQ ID NO: 3

257 <211> LENGTH: 29

258 <212> TYPE: DNA

259 <213> ORGANISM: HUMAN

261 <400> SEQUENCE: 3

262 cgcccagtggtgtcatcttcc ccagaagag

29

265 <210> SEQ ID NO: 4

266 <211> LENGTH: 19

267 <212> TYPE: DNA

268 <213> ORGANISM: HUMAN

270 <400> SEQUENCE: 4

271 ggaatcctcc tgcattccgg

19

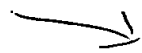
274 <210> SEQ ID NO: 5

275 <211> LENGTH: 10898

276 <212> TYPE: DNA

277 <213> ORGANISM: HUMAN

279 <220> FEATURE:



missing mandatory <220> to <223>
features to explain the "n" at
position 1974 in the sequence.

See #10 on the Error Summary Sheet.

Note: This error is indicated elsewhere
in the sequence listing. Please review
and correct.

VERIFICATION SUMMARY

DATE: 05/07/2001

PATENT APPLICATION: US/09/807,949

TIME: 14:23:59

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:316 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:512 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:688 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:702 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1371 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:58
L:1371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1804 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:90
L:1804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90
L:2064 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:110
L:2064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/807,949

DATE: 05/07/2001
TIME: 14:23:58

Input Set : A:\D-021-51.app
Output Set: N:\CRF3\05072001\1807949.raw

280 <221> NAME/KEY: gene
281 <222> LOCATION: (1)..(10898)
283 <400> SEQUENCE: 5

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285 ccactcaggg ttaaattgat taagggcggt gcaagatgtg ctttgtaaag cagatgcttg 120
286 aaggcagcat gctcgttaag agtcatcacc aatccctaatt ctcaagtaat cagggacaca 180
287 aacactgcgg aaggccgcag ggtcctctgc ctaggaaaac cagagacctt tgttcacttg 240
288 tttatctgac cttccctcca ctattgtcca tgaccctgcc aaatccccct ctgtgagaaa 300
289 caccacaaga ttatcaataa aaaaataaat ttaaaaaaaa aatacaaaaa aaaaaaaaaa 360
290 aaaaaaaaaa gacttacgaa tagttattga taaatgaata gctattggta aagccaagta 420
291 aatgatcata ttcaaaacca gacggccatc atcacagctc aagtctacct gatttgatct 480
292 ctttatcatt gtcattcttt ggattcacta gattagtcac catcctcaaa attctcccc 540
293 aagttctaatt tacgttccaa acatttaggg gttacatgaa gcttgaacct actaccttct 600
294 ttgcttttga gccatgagtt gtaggaatga tgagtttaca ccttacatgc tggggattaa 660
295 ttttttggat ttttggtaga gacggggttt caccgtgtta gccagaatgg tctcgatctc 720
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302 ttttttggat ttttggtaga gacggggttt caccgtgtta gccagaatgg tctcgatctc 1140
303 ctgacttcgt gatccacccg cctcggcctc ccaaagttct gggattacag gtgtgagcca 1200
304 ccgcacctgg ccaatttttt gagtctttta aagtaaaaat atgtcttgta agctggtaac 1260
305 tatggtacat ttctttttat taatgtggtg ctgacgggtc tataggttct tttgagtttg 1320
306 gcatgcataat gctacttttt gcagtccctt cattacattt ttctctcttc atttgaagag 1380
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315 ggttcataat ctcaattctg tcagaattgg tacaagaaat agctgctatg tttcttgaca 1920
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322 tatgatgata ttgacagggt ttgcccctac tcaactagatt gtgagctcct gctcagggca 2340
323 ggtagcgttt tttgtttttg tttttgtttt tcttttttga gacagggtct tgctctgtca 2400
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325 aaccatcatc caatttcagc ctctgagta gctgggacta caggcacatg ccattacacc 2520
326 tggctaattt ttttgtattt ctagttagaga cagggttttg ccattgtgcc cgggctggtc 2580
327 tcgaactcct ggactcaagc aatccaccca cctcagcctc ccaaaatgag ggaccgtgtc 2640
328 ttattcattt ccatgtccct agtccatagc ccagtgtgag acctatggta gtactaaata 2700
329 aatatttgtt gaatgcaata gtaaatagca tttcagggag caagaactag attaacaaa 2760

```

→ "n" at
position 1974
see previous
page.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.